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OIEP

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/877,804

TIME: 16:04:52

Input Set : A:\P0576PlC2.txt

Output Set: N:\CRF3\09182001\I877804.raw

ENTERED

3 <110> APPLICANT: Nikolics, Karoly
 4 McFarland, Keith C.
 5 Segalo, Deborah L.
 6 Seeburg, Peter H.
 8 <120> TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
 10 <130> FILE REFERENCE: P0576PlC2
 12 <140> CURRENT APPLICATION NUMBER: US 09/877,804
 C--> 13 <141> CURRENT FILING DATE: 2001-09-04
 15 <150> PRIOR APPLICATION NUMBER: US 08/207,814
 16 <151> PRIOR FILING DATE: 1994-03-07
 18 <150> PRIOR APPLICATION NUMBER: US 07/781,153
 19 <151> PRIOR FILING DATE: 1991-10-31
 21 <150> PRIOR APPLICATION NUMBER: US 07/347,683
 22 <151> PRIOR FILING DATE: 1989-05-05
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 27 <211> LENGTH: 2902
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Rattus
 31 <400> SEQUENCE: 1
 32 atactggctc aacctcggga gctcacactc aggctggcgg gcc atg 46
 33 Met
 34 1
 36 ggg cgg cga gtc cca gct ctg aga cag ctg ctg gtg ctg 85
 37 Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Leu Val Leu
 38 5 10
 40 gca gtg ctg ctg ctg aag cct tca cag ctg cag tcc cga 124
 41 Ala Val Leu Leu Leu Lys Pro Ser Gln Leu Gln Ser Arg
 42 15 20 25
 44 gag ctg tca ggg tcg cgc tgc ccc gag ccc tgc gac tgc 163
 45 Glu Leu Ser Gly Ser Arg Cys Pro Glu Pro Cys Asp Cys
 46 30 35 40
 48 gca ccg gat ggc gcc ctg cgc tgt cct ggc cct cga gcc 202
 49 Ala Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Arg Ala
 50 45 50
 52 ggc ctc gcc aga cta tct ctc acc tat ctc cct gtc aaa 241
 53 Gly Leu Ala Arg Leu Ser Leu Thr Tyr Leu Pro Val Lys
 54 55 60 65
 56 gta att cca tca caa gct ttc agg gga ctt aat gag gtc 280
 57 Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val
 58 70 75
 60 gta aaa att gaa atc tct cag agt gat tcc ctg gaa agg 319
 61 Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg
 62 80 85 90
 64 ata gaa gct aat gcc ttt gac aac ctc ctc aat ttg tct 358
 65 Ile Glu Ala Asn Ala Phe Asp Asn Leu Leu Asn Leu Ser
 66 95 100 105

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68  gaa cta ctg atc cag aac acc aaa aac ctg cta tac att 397
69  Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Leu Tyr Ile
70          110          115
72  gaa cct ggt gct ttt aca aac ctc cct cgg tta aaa tac 436
73  Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg Leu Lys Tyr
74          120          125          130
76  ctg agc atc tgt aac aca ggc atc cga acc ctt cca gat 475
77  Leu Ser Ile Cys Asn Thr Gly Ile Arg Thr Leu Pro Asp
78          135          140
80  gtt acg aag atc tcc tcc tct gaa ttt aat ttc att ctg 514
81  Val Thr Lys Ile Ser Ser Ser Glu Phe Asn Phe Ile Leu
82  145          150          155
84  gaa atc tgt gat aac tta cac ata acc acc ata ccc ggg 553
85  Glu Ile Cys Asp Asn Leu His Ile Thr Thr Ile Pro Gly
86          160          165          170
88  aat gct ttc caa ggg atg aat aac gag tct gtc aca cta 592
89  Asn Ala Phe Gln Gly Met Asn Asn Glu Ser Val Thr Leu
90          175          180
92  aaa ctg tat gga aat gga ttt gaa gaa gta caa agc cat 631
93  Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser His
94          185          190          195
96  gca ttc aat ggg acg act cta atc tcg ctg gag cta aaa 670
97  Ala Phe Asn Gly Thr Thr Leu Ile Ser Leu Glu Leu Lys
98          200          205
100 gaa aac atc tac ctg gag aag atg cac agt gga gcc ttc 709
101 Glu Asn Ile Tyr Leu Glu Lys Met His Ser Gly Ala Phe
102 210          215          220
104 cag ggg gcc acg ggg ccc agc atc ctg gat att tct tcc 748
105 Gln Gly Ala Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser
106 225          230          235
108 acc aaa ttg cag gcc ctg ccg agc cac ggg ctg gag tcc 787
109 Thr Lys Leu Gln Ala Leu Pro Ser His Gly Leu Glu Ser
110          240          245
112 att cag acg ctc atc gcc ctg tct tcc tac tca ctg aaa 826
113 Ile Gln Thr Leu Ile Ala Leu Ser Ser Tyr Ser Leu Lys
114 250          255          260
116 aca ctg ccc tcc aaa gaa aaa ttc acg agc ctc ctg gtc 865
117 Thr Leu Pro Ser Lys Glu Lys Phe Thr Ser Leu Leu Val
118          265          270
120 gcc acg ctg acc tac ccc agc cac tgc tgc gcc ttc agg 904
121 Ala Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg
122 275          280          285
124 aat ttg ccg aag aaa gaa cag aat ttt tca ttt tcc att 943
125 Asn Leu Pro Lys Lys Glu Gln Asn Phe Ser Phe Ser Ile
126 290          295          300
128 ttt gaa aac ttc tcc aaa caa tgc gaa agc aca gtt aga 982
129 Phe Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg
130          305          310
132 aaa gca gat aac gag acg ctt tat tcc gcc atc ttt gag 1021

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133  Lys Ala Asp Asn Glu Thr Leu Tyr Ser Ala Ile Phe Glu
134      315                      320                      325
136  gag aat gaa ctc agt ggc tgg gat tat gat tat ggc ttc 1060
137  Glu Asn Glu Leu Ser Gly Trp Asp Tyr Asp Tyr Gly Phe
138      330                      335
140  tgt tca ccc aag aca ctc caa tgt gct cca gaa cca gat 1099
141  Cys Ser Pro Lys Thr Leu Gln Cys Ala Pro Glu Pro Asp
142  340                      345                      350
144  gct ttc aac ccc tgt gaa gat att atg ggc tat gcc ttc 1138
145  Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Ala Phe
146      355                      360                      365
148  ctt agg gtc ctg att tgg ctg att aat ata cta gcc atc 1177
149  Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile
150      370                      375
152  ttt ggc aac ctg aca gtc ctc ttt gtt ctc ctg acc agt 1216
153  Phe Gly Asn Leu Thr Val Leu Phe Val Leu Leu Thr Ser
154      380                      385                      390
156  cgt tat aaa ctg aca gtg ccc cgc ttc ctc atg tgt aat 1255
157  Arg Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn
158      395                      400
160  ctc tcc ttt gca gac ttt tgc atg ggg ctc tac ctg ctg 1294
161  Leu Ser Phe Ala Asp Phe Cys Met Gly Leu Tyr Leu Leu
162  405                      410                      415
164  ctc att gcc tcc gtg gac tcc caa aca aaa ggc cag tac 1333
165  Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly Gln Tyr
166      420                      425                      430
168  tat aac cac gcc ata gac tgg cag aca ggg agt ggc tgc 1372
169  Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys
170      435                      440
172  ggt gca gct ggc ttc ttt act gtg ttt gcc agt gaa ctc 1411
173  Gly Ala Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu
174      445                      450                      455
176  tct gtc tac acc ctg acg gtt atc acc ctg gaa agg tgg 1450
177  Ser Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp
178      460                      465
180  cac acc atc acc tat gct gta cag cta gac caa aag cta 1489
181  His Thr Ile Thr Tyr Ala Val Gln Leu Asp Gln Lys Leu
182  470                      475                      480
184  aga ctg agg cat gcc atc cca att atg ctc gga gga tgg 1528
185  Arg Leu Arg His Ala Ile Pro Ile Met Leu Gly Gly Trp
186      485                      490                      495
188  ctc ttt tct acg ctg atc gcc acg atg ccc ctt gtg ggt 1567
189  Leu Phe Ser Thr Leu Ile Ala Thr Met Pro Leu Val Gly
190      500                      505
192  atc agc aat tac atg aag gtc agc atc tgc ctc ccc atg 1606
193  Ile Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met
194      510                      515                      520
196  gat gtg gaa tcc act ctg tcc caa gtc tac ata tta tcc 1645
197  Asp Val Glu Ser Thr Leu Ser Gln Val Tyr Ile Leu Ser

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198          525          530
200 atc tta atc ctc aac gtg gtg gcc ttc gtc gtc atc tgt 1684
201 Ile Leu Ile Leu Asn Val Val Ala Phe Val Val Ile Cys
202 535          540          545
204 gct tgc tac att agg atc tac ttt gca gtt caa aat cca 1723
205 Ala Cys Tyr Ile Arg Ile Tyr Phe Ala Val Gln Asn Pro
206          550          555          560
208 gag ctg aca gct cct aac aag gac aca aaa att gct aag 1762
209 Glu Leu Thr Ala Pro Asn Lys Asp Thr Lys Ile Ala Lys
210          565          570
212 aag atg gcc atc ctc atc ttc aca gac ttc acg tgc atg 1801
213 Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met
214          575          580          585
216 gcg ccc atc tct ttc ttt gcc atc tcg gct gcc ttc aaa 1840
217 Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys
218          590          595
220 gtg ccc ctt atc act gtc acc aac tcg aaa atc tta ctg 1879
221 Val Pro Leu Ile Thr Val Thr Asn Ser Lys Ile Leu Leu
222 600          605          610
224 gtc ctt ttt tat cct gtc aat tct tgt gcc aat cca ttt 1918
225 Val Leu Phe Tyr Pro Val Asn Ser Cys Ala Asn Pro Phe
226          615          620          625
228 ctg tat gcg atc ttc acg aag gcg ttt cag aga gat ttc 1957
229 Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Phe
230          630          635
232 ctt ctg ctg ctg agc cga ttc ggc tgc tgt aaa cgc cgg 1996
233 Leu Leu Leu Leu Ser Arg Phe Gly Cys Cys Lys Arg Arg
234          640          645          650
236 gcg gag ctt tac aga agg aag gaa ttt tct gca tat act 2035
237 Ala Glu Leu Tyr Arg Arg Lys Glu Phe Ser Ala Tyr Thr
238          655          660
240 tcc aac tgc aaa aat ggc ttc cca gga gca agt aag ccg 2074
241 Ser Asn Cys Lys Asn Gly Phe Pro Gly Ala Ser Lys Pro
242 665          670          675
244 tcc cag gct acc ctg aag ttg tcc aca gtg cac tgt caa 2113
245 Ser Gln Ala Thr Leu Lys Leu Ser Thr Val His Cys Gln
246          680          685          690
248 cag ccc ata cca ccg aga gcg tta act cac tagcatt 2150
249 Gln Pro Ile Pro Pro Arg Ala Leu Thr His
250          695          700
252 acaaaattgt gcctaaatat gttttttaaa aagtgtttta gaaaaatatt 2200
254 tatccttagg cacttcagga gaattgtacc tgcttcagag gacggcctat 2250
256 aacacttggt cacataagtt tcaggaaggt ttagaaatatt ttatagtaat 2300
258 ttaggcataa taattttttg ttgaatctaa tactaaggaa atctaagttg 2350
260 tcattttttca cgtctctgac attttttcatt tcaatcttgt gatttacatt 2400
262 gtaatctcca aatatattac ttcatagcag attgaaaatt taaactggtc 2450
264 ttgtcctca gatagtttga taaatatatt caagagatgc actgtgcagt 2500
266 gtgactgcta gccttgcatg gtaaatagaa gtttcttagc catattccaa 2550
268 gtgcttcaca tgtcacacta ggaggcacag atgcaaactg tttacatcag 2600

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270 tgaattctat tagccagctc tattctagag acttctatatt cccattgaca 2650
 272 ctctgcttaa ctttccatct gaaggcacat gctgcatatt tgtttggctt 2700
 274 acagatcatg agtacctcat ggccaggagc ccatctcagc ccatcttggt 2750
 276 cctcgtctat ctcaggatct tggaaatgct acacagcaag catgcctagc 2800
 278 cagttaaact ccctaaatct acacaggaaa atattttctac caccttagca 2850
 280 tattgttttc gatgattaca tgctttctgt attttgccct cctcctagta 2900
 282 tc 2902

284 <210> SEQ ID NO: 2

285 <211> LENGTH: 700

286 <212> TYPE: PRT

287 <213> ORGANISM: Artificial sequence

289 <220> FEATURE:

290 <223> OTHER INFORMATION: deduced sequence OK

292 <400> SEQUENCE: 2

293 Met Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Leu Val Leu Ala
 294 1 5 10 15
 296 Val Leu Leu Leu Lys Pro Ser Gln Leu Gln Ser Arg Glu Leu Ser
 297 20 25 30
 299 Gly Ser Arg Cys Pro Glu Pro Cys Asp Cys Ala Pro Asp Gly Ala
 300 35 40 45
 302 Leu Arg Cys Pro Gly Pro Arg Ala Gly Leu Ala Arg Leu Ser Leu
 303 50 55 60
 305 Thr Tyr Leu Pro Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly
 306 65 70 75
 308 Leu Asn Glu Val Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu
 309 80 85 90
 311 Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn Leu Leu Asn Leu Ser
 312 95 100 105
 314 Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Leu Tyr Ile Glu Pro
 315 110 115 120
 317 Gly Ala Phe Thr Asn Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys
 318 125 130 135
 320 Asn Thr Gly Ile Arg Thr Leu Pro Asp Val Thr Lys Ile Ser Ser
 321 140 145 150
 323 Ser Glu Phe Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile
 324 155 160 165
 326 Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met Asn Asn Glu Ser
 327 170 175 180
 329 Val Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser
 330 185 190 195
 332 His Ala Phe Asn Gly Thr Thr Leu Ile Ser Leu Glu Leu Lys Glu
 333 200 205 210
 335 Asn Ile Tyr Leu Glu Lys Met His Ser Gly Ala Phe Gln Gly Ala
 336 215 220 225
 338 Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala
 339 230 235 240
 341 Leu Pro Ser His Gly Leu Glu Ser Ile Gln Thr Leu Ile Ala Leu
 342 245 250 255
 344 Ser Ser Tyr Ser Leu Lys Thr Leu Pro Ser Lys Glu Lys Phe Thr

VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5